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RAW SEQUENCE LISTING

DATE: 11/20/2001

PATENT APPLICATION: US/09/965,522

TIME: 10:10:19

Input Set : N:\Crf3\RULE60\09965522.txt

Output Set: N:\CRF3\11202001\I965522.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Lal, Preeti

6 Bandman, Olga

8 (ii) TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT

9 PHOSPHATE CO-TRANSPORTER

11 (iii) NUMBER OF SEQUENCES: 7

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

15 (B) STREET: 3174 Porter Drive

16 (C) CITY: Palo Alto

17 (D) STATE: CA

18 (E) COUNTRY: US

19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette

23 (B) COMPUTER: IBM Compatible

24 (C) OPERATING SYSTEM: DOS

25 (D) SOFTWARE: FastSEQ Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/965,522

C--> 29 (B) FILING DATE: 26-Sep-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/391,958

34 (B) FILING DATE: 1999-09-08

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Billings, Lucy J.

39 (B) REGISTRATION NUMBER: 36,749

40 (C) REFERENCE/DOCKET NUMBER: PF-0221 US

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 415-855-0555

44 (B) TELEFAX: 415-845-4166

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 401 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (vii) IMMEDIATE SOURCE:

56 (A) LIBRARY: BRAITUT02

57 (B) CLONE: 754412

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

61 Met Gln Val Asp Glu Thr Leu Ile Pro Arg Lys Val Pro Ser Leu Cys

62 1 5 10 15

63 Ser Ala Arg Tyr Gly Ile Ala Leu Val Leu His Phe Cys Asn Phe Thr

64 20 25 30

ENTERED

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```

65 Thr Ile Ala Gln Asn Val Ile Met Asn Ile Thr Met Val Ala Met Val
66          35                      40                      45
67 Asn Ser Thr Ser Pro Gln Ser Gln Leu Asn Asp Ser Ser Glu Val Leu
68          50                      55                      60
69 Pro Val Asp Ser Phe Gly Gly Leu Ser Lys Ala Pro Lys Ser Leu Pro
70          65                      70                      75                      80
71 Ala Lys Ser Ser Ile Leu Gly Gly Gln Phe Ala Ile Trp Glu Arg Trp
72          85                      90                      95
73 Gly Pro Pro Gln Glu Arg Ser Arg Leu Cys Ser Ile Ala Leu Ser Gly
74          100                     105                     110
75 Met Leu Leu Gly Cys Phe Thr Ala Ile Leu Ile Gly Gly Phe Ile Ser
76          115                     120                     125
77 Glu Thr Leu Gly Trp Pro Phe Val Phe Tyr Ile Phe Gly Gly Val Gly
78          130                     135                     140
79 Cys Val Cys Cys Leu Leu Trp Phe Val Val Ile Tyr Asp Asp Pro Val
80          145                     150                     155                     160
81 Ser Tyr Pro Trp Ile Ser Thr Ser Glu Lys Glu Tyr Ile Ile Ser Ser
82          165                     170                     175
83 Leu Lys Gln Gln Val Gly Ser Ser Lys Gln Pro Leu Pro Ile Lys Ala
84          180                     185                     190
85 Met Leu Arg Ser Leu Pro Ile Trp Ser Ile Cys Leu Gly Cys Phe Ser
86          195                     200                     205
87 His Gln Trp Leu Val Ser Thr Met Val Val Tyr Ile Pro Thr Tyr Ile
88          210                     215                     220
89 Ser Ser Val Tyr His Val Asn Ile Arg Asp Asn Gly Leu Leu Ser Ala
90          225                     230                     235                     240
91 Leu Pro Phe Ile Val Ala Trp Val Ile Gly Met Val Gly Gly Tyr Leu
92          245                     250                     255
93 Ala Asp Phe Leu Leu Thr Lys Lys Phe Arg Leu Ile Thr Val Arg Lys
94          260                     265                     270
95 Ile Ala Thr Ile Leu Gly Ser Leu Pro Ser Ser Ala Leu Ile Val Ser
96          275                     280                     285
97 Leu Pro Tyr Leu Asn Ser Gly Tyr Ile Thr Ala Thr Ala Leu Leu Thr
98          290                     295                     300
99 Leu Ser Cys Gly Leu Ser Thr Leu Cys Gln Ser Gly Ile Tyr Ile Asn
100         305                     310                     315                     320
101 Val Leu Asp Ile Ala Pro Arg Tyr Ser Ser Phe Leu Met Gly Ala Ser
102          325                     330                     335
103 Arg Gly Phe Ser Ser Ile Ala Pro Val Ile Val Pro Thr Val Ser Gly
104          340                     345                     350
105 Phe Leu Leu Ser Gln Asp Pro Glu Phe Gly Trp Arg Asn Val Phe Phe
106          355                     360                     365
107 Leu Leu Phe Ala Val Asn Leu Leu Gly Leu Leu Phe Tyr Leu Ile Phe
108          370                     375                     380
109 Gly Glu Ala Asp Val Gln Glu Trp Ala Lys Glu Arg Lys Leu Thr Arg
110          385                     390                     395                     400
111 Leu
114 (2) INFORMATION FOR SEQ ID NO: 2:
116 (i) SEQUENCE CHARACTERISTICS:

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```

117      (A) LENGTH: 1643 base pairs
118      (B) TYPE: nucleic acid
119      (C) STRANDEDNESS: single
120      (D) TOPOLOGY: linear
122      (vii) IMMEDIATE SOURCE:
123          (A) LIBRARY: BRAITUT02
124          (B) CLONE: 754412
126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128      AGAACGGTGA GGATGACCGA CGTATAGGCG AGAGCCTAGG TACGCCATGC CAGGTCACCG      60
129      GTCCGGCAAT TCCCGGGTCG ACCCAGCGGT CCGCTTGGAG GGACGCTGGG TTCAACTTGA      120
130      AGCCCTTCCA CAGACATTAA GTCGGTGAAA ACCATTCACT AGGAGAGGAG AAACACAATG      180
131      GCCACCAAGA CAGAGTTGAG TCCACAGCA AGGGAGAGCA AGAACGCACA AGATATGCAA      240
132      GTGGATGAGA CACTGATCCC CAGGAAAAGTT CCAAGTTTAT GTTCTGCTCG CTATGGAATA      300
133      GCCCTCGTCT TACATTTCTG CAATTTTACA ACGATAGCAC AAAATGTCAT CATGAACATC      360
134      ACCATGGTAG CCATGGTCAA CAGCACAAGC CCTCAATCCC AGCTCAATGA TTCTCTGAG      420
135      GTGCTGCCTG TTGACTCATT TGGTGGCCTA AGTAAAGCCC CAAAGAGTCT TCCTGCAAAG      480
136      TCCTCAATAC TTGGGGGTCA GTTTGCAATT TGGGAAAGGT GGGGCCCTCC ACAAGAACGA      540
137      AGCAGACTCT GCAGCATTGC TTTATCAGGA ATGTTACTGG GATGCTTTAC TGCCATCCTC      600
138      ATAGGTGGCT TCATTAGTGA AACCCTTGGG TGGCCCTTTG TCTTCTATAT CTTTGGAGGT      660
139      GTTGGCTGTG TCTGCTGCCT TCTCTGGTTT GTTGTGATTT ATGATGACCC CGTTTCCTAT      720
140      CCATGGATAA GCACCTCAGA AAAAGAATAC ATCATATCCT CCTTGAAACA ACAGGTCGGG      780
141      TCTTCTAAGC AGCCTCTTCC CATCAAAGCT ATGCTCAGAT CTCTACCCAT TTGGTCCATA      840
142      TGTTTAGGCT GTTTCAGCCA TCAATGGTTA GTTAGCACAA TGGTTGTATA CATACCAACT      900
143      TACATCAGCT CTGTGTACCA TGTTAACATC AGAGACAATG GACTTCTATC TGCCCTTCCT      960
144      TTTATTGTTG CCTGGGTCAT AGGCATGGTG GGAGGCTATC TGGCAGATTT CCTTCTAACC      1020
145      AAAAAGTTTA GACTCATCAC TGTGAGGAAA ATTGCCACAA TTTTAGGAAG TCTCCCCTCT      1080
146      TCAGCACTCA TTGTGTCTCT GCCTTACCTC AATTCCGGCT ATATCACAGC AACTGCCTTG      1140
147      CTGACGCTCT CTTGCGGATT AAGCACATTG TGTCACTCAG GGATTTATAT CAATGCTCTTA      1200
148      GATATTGCTC CAAGGTATTG CAGTTTTCTC ATGGGAGCAT CAAGAGGATT TTCGAGCATA      1260
149      GCACCTGTCA TTGTACCCAC TGTCAGCGGA TTTCTTCTTA GTCAGGACCC TGAGTTTGGG      1320
150      TGGAGGAATG TCTTCTTCTT GCTGTTTGCC GTTAACTGTG TAGGACTACT CTTCTACCTC      1380
151      ATATTTGGAG AAGCAGATGT CCAAGAATGG GCTAAAGAGA GAAAACTCAC TCGTTTATGA      1440
152      AGTTATCCCA CCTTGGATGG AAAAGTCATT AGGCACCGTA TTGCATAAAA TAGAAGGCTT      1500
153      CCGTGATGAA AATACCAGTG AAAAGATTTT TTTTCTCTGT GGCTCTTTTC AATTATGAGA      1560
154      TCAGTTCATT ATTTTATTCA GACTTTTTTT TGAGAGAAAT GTAAGATGAA TAAAAATTCA      1620
155      AATAAAATGA TAACTAAGAA TGC      1643
157      (2) INFORMATION FOR SEQ ID NO: 3:
159          (i) SEQUENCE CHARACTERISTICS:
160              (A) LENGTH: 467 amino acids
161              (B) TYPE: amino acid
162              (C) STRANDEDNESS: single
163              (D) TOPOLOGY: linear
165          (vii) IMMEDIATE SOURCE:
166              (A) LIBRARY: GenBank
167              (B) CLONE: 450532
169          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
171      Met Gln Met Asp Asn Arg Leu Pro Pro Lys Lys Val Pro Gly Phe Cys
172      1          5          10          15
173      Ser Phe Arg Tyr Gly Leu Ser Phe Leu Val His Cys Cys Asn Val Ile

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 174 | | 20 | | 25 | | 30 | | | | | | | | | | |
| 175 | Ile | Thr | Ala | Gln | Arg | Ala | Cys | Leu | Asn | Leu | Thr | Met | Val | Val | Met | Val |
| 176 | | | 35 | | | | | 40 | | | | | 45 | | | |
| 177 | Asn | Ser | Thr | Asp | Pro | His | Gly | Leu | Pro | Asn | Thr | Ser | Thr | Lys | Lys | Leu |
| 178 | | | 50 | | | | 55 | | | | | 60 | | | | |
| 179 | Leu | Asp | Asn | Ile | Lys | Asn | Pro | Met | Tyr | Asn | Trp | Ser | Pro | Asp | Ile | Gln |
| 180 | 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| 181 | Gly | Ile | Ile | Leu | Ser | Ser | Thr | Ser | Tyr | Gly | Val | Ile | Ile | Ile | Gln | Val |
| 182 | | | | | 85 | | | | | 90 | | | | | 95 | |
| 183 | Pro | Val | Gly | Tyr | Phe | Ser | Gly | Ile | Tyr | Ser | Thr | Lys | Lys | Met | Ile | Gly |
| 184 | | | 100 | | | | | | 105 | | | | | 110 | | |
| 185 | Phe | Ala | Leu | Cys | Leu | Ser | Ser | Val | Leu | Ser | Leu | Leu | Ile | Pro | Pro | Ala |
| 186 | | | 115 | | | | | 120 | | | | | 125 | | | |
| 187 | Ala | Gly | Ile | Gly | Val | Ala | Trp | Val | Val | Val | Cys | Arg | Ala | Val | Gln | Gly |
| 188 | | 130 | | | | | 135 | | | | 140 | | | | | |
| 189 | Ala | Ala | Gln | Gly | Ile | Val | Ala | Thr | Ala | Gln | Phe | Glu | Ile | Tyr | Val | Lys |
| 190 | 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| 191 | Trp | Ala | Pro | Pro | Leu | Glu | Arg | Gly | Arg | Leu | Thr | Ser | Met | Ser | Thr | Ser |
| 192 | | | | | 165 | | | | | 170 | | | | | 175 | |
| 193 | Gly | Phe | Leu | Leu | Gly | Pro | Phe | Ile | Val | Leu | Leu | Val | Thr | Gly | Val | Ile |
| 194 | | | 180 | | | | | | 185 | | | | | 190 | | |
| 195 | Cys | Glu | Ser | Leu | Gly | Trp | Pro | Met | Val | Phe | Tyr | Ile | Phe | Gly | Ala | Cys |
| 196 | | | 195 | | | | | 200 | | | | | 205 | | | |
| 197 | Gly | Cys | Ala | Val | Cys | Leu | Leu | Trp | Phe | Val | Leu | Phe | Tyr | Asp | Asp | Pro |
| 198 | | 210 | | | | | 215 | | | | | 220 | | | | |
| 199 | Lys | Asp | His | Pro | Cys | Ile | Ser | Ile | Ser | Glu | Lys | Glu | Tyr | Ile | Thr | Ser |
| 200 | 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| 201 | Ser | Leu | Val | Gln | Gln | Val | Ser | Ser | Ser | Arg | Gln | Ser | Leu | Pro | Ile | Lys |
| 202 | | | | | 245 | | | | | 250 | | | | | 255 | |
| 203 | Ala | Ile | Leu | Lys | Ser | Leu | Pro | Val | Trp | Ala | Ile | Ser | Ile | Gly | Ser | Phe |
| 204 | | | 260 | | | | | | 265 | | | | | 270 | | |
| 205 | Thr | Phe | Phe | Trp | Ser | His | Asn | Ile | Met | Thr | Leu | Tyr | Thr | Pro | Met | Phe |
| 206 | | | 275 | | | | | 280 | | | | | 285 | | | |
| 207 | Ile | Asn | Ser | Met | Leu | His | Val | Asn | Ile | Lys | Glu | Asn | Gly | Phe | Leu | Ser |
| 208 | | 290 | | | | 295 | | | | | 300 | | | | | |
| 209 | Ser | Leu | Pro | Tyr | Leu | Phe | Ala | Trp | Ile | Cys | Gly | Asn | Leu | Ala | Gly | Gln |
| 210 | 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| 211 | Leu | Ser | Asp | Phe | Phe | Leu | Thr | Arg | Asn | Ile | Leu | Ser | Val | Ile | Ala | Val |
| 212 | | | | 325 | | | | | | 330 | | | | | 335 | |
| 213 | Arg | Lys | Leu | Phe | Thr | Ala | Ala | Gly | Phe | Leu | Leu | Pro | Ala | Ile | Phe | Gly |
| 214 | | | 340 | | | | | | 345 | | | | | 350 | | |
| 215 | Val | Cys | Leu | Pro | Tyr | Leu | Ser | Ser | Thr | Phe | Tyr | Ser | Ile | Val | Ile | Phe |
| 216 | | | 355 | | | | | 360 | | | | | 365 | | | |
| 217 | Leu | Ile | Leu | Ala | Gly | Ala | Thr | Gly | Ser | Phe | Cys | Leu | Gly | Gly | Val | Phe |
| 218 | | 370 | | | | 375 | | | | | | 380 | | | | |
| 219 | Ile | Asn | Gly | Leu | Asp | Ile | Ala | Pro | Arg | Tyr | Phe | Gly | Phe | Ile | Lys | Ala |
| 220 | 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| 221 | Cys | Ser | Thr | Leu | Thr | Gly | Met | Ile | Gly | Gly | Leu | Ile | Ala | Ser | Thr | Leu |
| 222 | | | | 405 | | | | | 410 | | | | | | 415 | |

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223 Thr Gly Leu Ile Leu Lys Gln Asp Pro Glu Ser Ala Trp Phe Lys Thr
224           420           425           430
225 Phe Ile Leu Met Ala Ala Ile Asn Val Thr Gly Leu Ile Phe Tyr Leu
226           435           440           445
227 Ile Val Ala Thr Ala Glu Ile Gln Asp Trp Ala Lys Glu Lys Gln His
228           450           455           460
229 Thr Arg Leu
230 465
232 (2) INFORMATION FOR SEQ ID NO: 4:
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 560 amino acids
236 (B) TYPE: amino acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear
240 (vii) IMMEDIATE SOURCE:
241 (A) LIBRARY: GenBank
242 (B) CLONE: 507415
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
246 Met Glu Phe Arg Gln Glu Glu Phe Arg Lys Leu Ala Gly Arg Ala Leu
247 1           5           10           15
248 Gly Arg Leu His Arg Leu Leu Glu Lys Arg Gln Glu Gly Ala Glu Thr
249           20           25           30
250 Leu Glu Leu Ser Ala Asp Gly Arg Pro Val Thr Thr His Thr Arg Asp
251           35           40           45
252 Pro Pro Val Val Asp Cys Thr Cys Phe Gly Leu Pro Arg Arg Tyr Ile
253           50           55           60
254 Ile Ala Ile Met Ser Gly Leu Gly Phe Cys Ile Ser Phe Gly Ile Arg
255           65           70           75           80
256 Cys Asn Leu Gly Val Ala Ile Val Ser Met Val Asn Asn Ser Thr Thr
257           85           90           95
258 His Arg Gly Gly His Val Val Val Gln Lys Ala Gln Phe Asn Trp Asp
259           100          105          110
260 Pro Glu Thr Val Gly Leu Ile His Gly Ser Phe Phe Trp Gly Tyr Ile
261           115          120          125
262 Val Thr Gln Ile Pro Gly Gly Phe Ile Cys Gln Lys Phe Ala Ala Asn
263           130          135          140
264 Arg Val Phe Gly Phe Ala Ile Val Ala Thr Ser Thr Leu Asn Met Leu
265           145          150          155          160
266 Ile Pro Ser Ala Ala Arg Val His Tyr Gly Cys Val Ile Phe Val Arg
267           165          170          175
268 Ile Leu Gln Gly Leu Val Glu Gly Val Thr Tyr Pro Ala Cys His Gly
269           180          185          190
270 Ile Trp Ser Lys Trp Ala Pro Pro Leu Glu Arg Ser Arg Leu Ala Thr
271           195          200          205
272 Thr Ala Phe Cys Gly Ser Tyr Ala Gly Ala Val Val Ala Met Pro Leu
273           210          215          220
274 Ala Gly Val Leu Val Gln Tyr Ser Gly Trp Ser Ser Val Phe Tyr Val
275           225          230          235          240
276 Tyr Gly Ser Phe Gly Ile Phe Trp Tyr Leu Phe Trp Leu Leu Val Ser

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]